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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:35:15 ; Search time 10 seconds

(without alignments)
49.772 Million cell updates/sec

Title: US-09-551-151A-43

Sequence: 1 SPQIAGORNFN 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 934

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	39.1	10	1	FARC_CALVO
2	24	37.5	9	1	TRP4_LEUMA
3	22	34.4	17	1	TRP2_LEUMA
4	21	32.8	14	1	SMSI_MYOSC
5	20	31.2	9	1	SMS_ALMT
6	20	31.2	17	1	TKL1_LOEMI
7	20	31.2	17	1	MDH_ACIDE
8	19	29.7	9	1	PRAD_CALVO
9	19	29.7	10	1	PCCK_FASHE
10	19	29.7	14	1	UN37_CLOPA
11	19	29.7	15	1	CIOA_RAT
12	19	29.7	17	1	FLAW_AZOOH
13	19	29.7	18	1	AZM_OCTIV
14	18	28.1	9	1	OXYT_RAUCI
15	18	28.1	11	1	CEP1_ACHFU
16	18	28.1	14	1	FLIB_MANLE
17	18	28.1	15	1	LECB_PSOSC
18	18	28.1	15	1	CBPB_PROAT
19	18	28.1	15	1	LECI_PSOSC
20	18	28.1	15	1	LECI_PSOSC
21	18	28.1	15	1	LECI_PSOSC
22	18	28.1	16	1	LECI_PSOSC
23	18	28.1	16	1	LECI_PSOSC
24	18	28.1	16	1	LECI_PSOSC
25	18	28.1	16	1	LECI_PSOSC
26	18	28.1	16	1	LECI_PSOSC
27	18	28.1	16	1	LECI_PSOSC
28	18	28.1	16	1	LECI_PSOSC
29	18	28.1	16	1	LECI_PSOSC
30	18	28.1	16	1	LECI_PSOSC
31	18	28.1	16	1	LECI_PSOSC
32	18	28.1	16	1	LECI_PSOSC
33	18	28.1	16	1	LECI_PSOSC

34	16	25.0	10	1	TRP9_LEUMA
35	16	25.0	10	1	URAI_HUMAN
36	16	25.0	11	1	RANC_RANPI
37	16	25.0	13	1	LIGB_TRAVE
38	16	25.0	13	1	TAI3_TREME
39	16	25.0	14	1	SODN_STRCR
40	16	25.0	16	1	MDH_SYNY4
41	16	25.0	16	1	PPAC_BACME
42	16	25.0	17	1	PNOC_PIG
43	16	25.0	18	1	AGI_EUPMA
44	15.5	24.2	10	1	TKL3_LOEMI
45	15	23.4	7	1	IGAO_DACDE

ALIGNMENTS

RESULT 1	FARC_CALVO	STANDARD;	PRT;	10 AA.
ID	FARC_CALVO			
AC	P41867;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	01-NOV-1995 (Rel. 32, Last annotation update)			
DE	Calliphoridae 12.			
OS	Calliphora vomitoria (Blue blowfly).			
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;			
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;			
OC	Muscomorpha; Oestroidea; Calliphoridae; Calliphora.			
OX	NCBI_TaxID=27454;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Thoracic ganglion;			
RA	MEDLINE=92196111; PubMed=1549595;			
RA	Duve H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,			
RA	Rehfeld J.F., Thorpe A.;			
RT	"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2			
RT	neuropeptides (designated calliphorin) from the blowfly			
RT	Calliphora vomitoria."			
RL	Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).			
CC	-1- SIMILARITY: BELONGS TO THE FARP (FARFAMIDE RELATED PEPTIDE)			
CC	FAMILY.			
DR	PIR; C44787; C44787.			
KM	Neuropeptide; Amidation.			
FT	MOD RES 10 10			
SO	SEQUENCE 10 AA; 1156 MW; 22810399C44AB6D8 CRC64;			
QY	6 AGORNF 11			
DB	2 AGDNF 7			
Query Match	39.1%; Score 25; DB 1; Length 10;			
Best local Similarity	83.3%; Pred. No. 66;			
Matches	5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
RESULT 2	TRP4_LEUMA	STANDARD;	PRT;	9 AA.
ID	TRP4_LEUMA			
AC	P81736;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Tachykinin-related peptide 4 (LeuTRP 4).			
OS	Leucophaea maderae (Mediterranean cockroach).			
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;			
OC	Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;			
OC	Blattelloidea; Blattellidae; Leucophaea.			
OX	NCBI_TaxID=6988;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Midgut;			
RX	MEDLINE=97053012; PubMed=8897641;			

RA Muren J.E., Naessel D.R.:
RT Isolation of five tachykinin-related peptides from the midgut of
the cockroach *Leucophaea maderae*: existence of N-terminally extended
isoforms.";
RL Regul. Pept. 65:185-196(1996).
CC -1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -1- TISSUE SPECIFICITY: MIDGUT.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 9 AA; 953 MW; 2403987699C865A7 CRC64;
SQ SEQUENCE 9 AA; 1798 MW; 485779A57F4221E3 CRC64;
Query Match 37.5%; Score 24; DB 1; Length 9;
Best Local Similarity 44.4%; Pred. No. 1,1e+05;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 SPOGIAGOR 9
DB 1 APSGFLGVR 17

RESULT 3
TRP2_LEUMA STANDARD; PRT; 17 AA.
ID TRP2_LEUMA STANDARD; PRT; 17 AA.
AC P81733; P81734;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tachykinin-related peptide 2 (leumrp 2) (Contains: Tachykinin-related
peptide 1 (leumrp 1)).
OS Leucophaea maderae (Mediterranean cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthoptera; Dictyoptera; Blattaria;
OC Blaberidae; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE-Midgut;
RX MEDLINE=97053012; PubMed=8897641;
RA Muren J.E., Naessel D.R.:
RT "Isolation of five tachykinin-related peptides from the midgut of
the cockroach *Leucophaea maderae*: existence of N-terminally extended
isoforms.";
RL Regul. Pept. 65:185-196(1996).
RN [2]
RP CHARACTERIZATION, AND MASS SPECTROMETRY.
RC TISSUE-Brain;
RX MEDLINE=97269266; PubMed=9114447;
RA Muren J.E., Naessel D.R.:
RT "Seven tachykinin-related peptides isolated from the brain of the
Leucophaea maderae cockroach: evidence for tissue-specific expression of
isoforms.";
RL Regul. Pept. 65:185-196(1996).
RN [3]
RP FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -1- TISSUE SPECIFICITY: MIDGUT AND BRAIN.
CC -1- MASS SPECTROMETRY: MW=1796.4; METHOD-MALDI; RANGE=1-17.
CC -1- MASS SPECTROMETRY: MW=903.1; METHOD-MALDI; RANGE=9-17.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT PEPTIDE 1 17 TACHYKININ-RELATED PEPTIDE 2.
FT PEPTIDE 9 17 TACHYKININ-RELATED PEPTIDE 1.
FT MOD_RES 17 17 AMIDATION.
SQ SEQUENCE 17 AA; 1798 MW; 485779A57F4221E3 CRC64;
Query Match 34.4%; Score 22; DB 1; Length 17;
Best Local Similarity 44.4%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 SPOGIAGOR 9
DB 9 APSGFLGVR 17

RESULT 4
SMS1_MYOSC STANDARD; PRT; 14 AA.
ID SMS1_MYOSC STANDARD; PRT; 14 AA.
AC P20750;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin I.
OS Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin),
Oncorhynchus kisutch (Coho salmon), and
Anguilla anguilla (European freshwater eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorphi; Scorpaeniformes;
OC Cottidae; Cottidae; Myoxocephalus.
OX NCBI_TaxID=8097, 8019, 7936;
RN [1]
RP SEQUENCE.
RC SPECIES-M.scorpius; TISSUE-Pancreas;
RX MEDLINE=88029486; PubMed=2889597;
RA Conlon J.M., Davis M.S., Falkner S., Thim L.;
RT "Structural characterization of peptides derived from
prosomatostatin I and II isolated from the pancreatic islets of two
species of teleostean fish: the daddy sculpin and the flounder.";
RL Eur. J. Biochem. 168:647-652(1987).
RN [2]
RP SEQUENCE.
RC SPECIES-O.kisutch; TISSUE-Pancreas;
RX MEDLINE=87055212; PubMed=2877919;
RA Plisetskaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,
Kimmel J.R., Andrews P.C., Gorman A.;
RT "Characterization of coho salmon (*Oncorhynchus kisutch*), islet
somatostatins.";
RL Gen. Comp. Endocrinol. 63:252-263(1986).
RN [3]
RP SEQUENCE.
RC SPECIES-A.anguilla; TISSUE-Pancreas;
RX MEDLINE=89065329; PubMed=2904391;
RA Conlon J.M., Deacon C.F., Hazen N., Henderson I.W., Thim L.;
RT "Somatostatin-related and glucagon-related peptides with unusual
structural features from the European eel (*Anguilla anguilla*).";
RL Gen. Comp. Endocrinol. 72:181-189(1988).
CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
DR PIR: S00172; S00172.
DR PIR: B60842; B60842.
DR PIR: A60840; A60840.
DR InterPro: IPR004250; Somatostatin.
DR Pfam: PF03002; Somatostatin; 1.
KW Hormone; Multigene family.
FT DISULFID 3 14
SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;
Query Match 32.8%; Score 21; DB 1; Length 14;
Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 6 AGORNE 11
DB 1 AGCKNF 6

RESULT 5
SMS_ALIMI STANDARD; PRT; 14 AA.
ID SMS_ALIMI STANDARD; PRT; 14 AA.
AC P31885;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin-14.

OS Alligator mississippiensis (American alligator), and
 OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496, 34903;
 RN [1]
 RN SEQUENCE.

RC SPECIES=Alligator mississippiensis; TISSUE=Stomach;
 RA MEDLINE=93324451; PubMed=8101369;
 RX Wang Y., Conlon J.M.;
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
 RT and stomach of the alligator.";
 RL Peptides 14:573-579(1993).
 RN [2]
 RN SEQUENCE.

RC SPECIES=T.scripita;
 RX MEDLINE=90341082; PubMed=1974347;
 RA Conlon J.M., Hicks J.W.;
 RT "Isolation and structural characterization of insulin, glucagon and
 RT somatostatin from the turtle, Pseudemys scripta.";
 RL Peptides 11:461-466(1990).
 CC -1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
 DR InterPro: IPR004250; Somatostatin.
 DR Pfam: PF03002; Somatostatin; 1.
 KW Hormone.
 FT DISULFID
 SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CMC64;

Query Match 32.8%; Score 21; DB 1; Length 14;
 Best Local Similarity 66.7%; Pred. No. 5.4e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 ACORNF 11
 Db 1 AGCKNF 6

RESULT 6
 ID TKL1_LOCM1 STANDARD; PRT; 9 AA.
 AC P16223;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Locustachykinin I (TK-1).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridoidea; Acrididae; Acridinae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RN SEQUENCE.
 RP TISSUE=Brain;
 RX MEDLINE=90184489; PubMed=2311766;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Locustachykinin I and II, two novel insect neuropeptides with
 RT homology to peptides of the vertebrate tachykinin family.";
 RL FEBS Lett. 261:397-401(1990).
 CC -1- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
 CC OVIDUCT AND FOREGUT.
 CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 DR PIR: S08265; ECLQIM.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 939 MW; 2389C86B59C865A7 CRC64;

Query Match 31.2%; Score 20; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 POGIACOR 9
 Db 2 POGIACOR 9

RESULT 7
 ID MDH_ACIDE STANDARD; PRT; 17 AA.
 AC P80540;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Malate dehydrogenase (EC 1.1.1.37) (Fragment).
 GN MDH.
 OS Acidovorax delafieldii.
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;
 OC Acidovorax.
 OX NCBI_TaxID=47920;
 RN [1]
 RN SEQUENCE.

RC STRAIN=CCUG 12929;
 RX MEDLINE=97334132; PubMed=9190829;
 RA Charnock C.;
 RT "Structural studies of malate dehydrogenases (MDHs): MDHs in
 RT Brevundimonas species are the first reported MDHs in Proteobacteria
 RT which resemble lactate dehydrogenases in primary structure.";
 RL J. Bacteriol. 179:4066-4070(1997).
 CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) -> oxaloacetate + NADH.
 CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
 DR InterPro: IPR01252; Mdh.
 DR PROSITE: PS00068; MDH; PARTIAL.
 DR Oxidoreductase; Tricarboxylic acid cycle; NAD.
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 1662 MW; 110E811A516999E CRC64;

Query Match 31.2%; Score 20; DB 1; Length 17;
 Best Local Similarity 80.0%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 GIAGO 8
 Db 11 GAGQ 15

RESULT 8
 ID FARD_CALVO STANDARD; PRT; 9 AA.
 AC P41868;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Calliphoridae 13.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Oestroidea; Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RN SEQUENCE.
 RP TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated calliphorin) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR PIR: D44787; D44787.
 DR Neuropeptide; Amidation.
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 1028 MW; 22D10693C87AB6D8 CRC64;

Query Match 29.7%; Score 19; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 AGORNF 11
 1111
 DB 1 AGODGF 6

RESULT 9
 PPCK_FASHE STANDARD; PRT; 10 AA.
 ID PPCK_FASHE
 AC P80525;
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Putative phosphoenolpyruvate carboxylase [GTP] (EC 4.1.1.32)
 DE (Phosphoenolpyruvate carboxylase) (PEPCK) (Newly excysted juvenile protein 1) (Fragment).
 OS Fasciola hepatica (liver fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Echinostomida; Echinostomata; Fascioloidae; Fasciola.
 OX NCBI_TaxID=6192;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95366993; PubMed=7639732;
 RA Tkalecic J., Ashman K., Meusen E.;
 RT Fasciola hepatica: rapid identification of newly excysted juvenile proteins.
 RL Biochem. Biophys. Res. Commun. 213:169-174(1995).
 CC -1 CARBOLYTIC ACTIVITY: GTP + oxaloacetate - GDP + phosphoenolpyruvate + CO(2).
 CC -1 SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP] FAMILY.
 CC DR InterPro: IPR000364; PEP_carboxykin.
 CC DR PROSITE: PS00505; PEPCK_GTP; PARTIAL.
 KW Lyase; Decarboxylase; GTP-binding.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1069 MW; 8393A6187A9C87A CRC64;

Query Match 29.7%; Score 19; DB 1; Length 10;
 Best Local Similarity 42.9%; Pred. No. 9.2e+02;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 POGIAC 8
 1111
 DB 2 PDGFDE 8

RESULT 10
 UN37_CLOPA STANDARD; PRT; 14 AA.
 ID UN37_CLOPA
 AC P81358;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Unknown protein CP 37 from 2D-page (Fragment).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RX STRAIN=M5;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flensburg R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5.";
 RL Electrophoresis 19:802-806(1998).
 CC -1 MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.8, ITS MW IS: 44.7 kDa.
 FT NON_TER 14

SQ SEQUENCE 14 AA; 1579 MW; 05384662DEF99210 CRC64;

Query Match 29.7%; Score 19; DB 1; Length 14;
 Best Local Similarity 60.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 QGIAG 7
 1111
 DB 10 QGVKG 14

RESULT 11
 C1QA_RAT STANDARD; PRT; 15 AA.
 ID C1QA_RAT
 AC P31720;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Complement C1q subcomponent, A chain (fragment).
 GN C1QA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93218657; PubMed=8464426;
 RA Wing M.G., Selly D.J., Bridgman D.J., Harrison R.A.;
 RT "Rapid isolation and biochemical characterization of rat C1 and C1q.";
 RL Mol. Immunol. 30:433-440(1993).
 CC -1 FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES C1R AND C1S TO YIELD C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+)-DEPENDENT C1R(2)C1S(2) PROENZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1 TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.
 CC -1 SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R AND S IN THE MOLAR RATION OF 1:2:2. THE C1Q SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE A AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE C CHAIN. IN ADDITION TO THE MAJOR A:B AND C:C DIMER BANDS, RAT, UNLIKE HUMAN C1Q, CONTAINED MINOR DIMER SPECIES.
 CC -1 SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
 CC DR InterPro: IPR001073; C1q.
 CC DR PROSITE: PS01113; C1Q; PARTIAL.
 KW Complement pathway; Plasma; Hydroxylation; Glycoprotein; Collagen; Repeat.
 FT DISULFID 15
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1488 MW; 1B3D8000B7793965 CRC64;

Query Match 29.7%; Score 19; DB 1; Length 15;
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 GTAG 7
 1111
 DB 12 GVAG 15

RESULT 12
 FLAM_AZOCH STANDARD; PRT; 17 AA.
 ID FLAM_AZOCH
 AC P23002;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Flavodoxin A (FLDA) (Fragment).
 OS Azotobacter chroococcum mod 1.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Azotobacter.
 OX NCBI_TaxID=355;
 RN [1]

RC STRAIN-MCD 1155; PubMed=1859358;
 RA MEDLINE-91315397; PubMed=1859358;
 RA Bagby S., Barker P.D., Hill H.A.O., Sanghera G.S., Dunbar B.,
 RA Ashby G.A., Eady R.R., Thorneley R.N.F.;
 RT "Direct electrochemistry of two genetically distinct flavodoxins
 RT isolated from *Asotobacter chroococcum* grown under nitrogen-fixing
 RT conditions.";
 RL Biochem. J. 277:313-319(1991).
 CC -1- FUNCTION: LOW-POTENTIAL ELECTRON DONOR TO A NUMBER OF REDOX
 CC ENZYMES.
 CC -1- COFACTOR: FMN.
 CC -1- SIMILARITY: BELONGS TO THE FLAVODOXIN FAMILY.
 DR InterPro: IPR001226; Flavodoxin.
 DR PROSITE: PS00201; FLAVODOXIN; PARTIAL.
 KW Electron transport; Flavoprotein; FMN.
 FT NON_TER 17
 FT THIOLEST 17
 SQ SEQUENCE 17 AA; 1692 MW; DE7B6DA36B24C7 CRC64;

Query Match 29.7%; Score 19; DB 1; Length 17;
 Best Local Similarity 37.5%; Pred. No. 1.6e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 SPOGIACO 8
 Db 9 SSSCVTKR 16

RESULT 13
 A2M_OCTVU STANDARD; PRT; 18 AA.
 ID P30800;
 AC 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2-macroglobulin homolog (Alpha-2-M) (fragment).
 OS Octopus vulgaris (Octopus).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
 OC Incirrata; Octopodidae; Octopus.
 OX NCBI_TaxID=6645;
 RN [1]
 RP SEQUENCE:
 RA MEDLINE-92344633; PubMed=1379044;
 RA Thøgersen I.B., Salvesen G., Brucato F.H., Pizzo S.V., Engblid J.J.;
 RT "Purification and characterization of an alpha-macroglobulin
 RT proteinase inhibitor from the mollusc *Octopus vulgaris*.";
 RL Biochem. J. 285:521-527(1992).
 CC -1- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A
 CC UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH,
 CC CALLED THE "BAIT REGION", WHICH CONTAINS SPECIFIC CLEAVAGE SITES
 CC FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT
 CC REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH
 CC TRAPS THE PROTEINASE. THE ENTRAPPED ENZYME REMAINS ACTIVE AGAINST
 CC LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR
 CC WEIGHT SUBSTRATES IS GREATLY REDUCED). FOLLOWING CLEAVAGE IN THE
 CC BAIT REGION A THIOLESTER BOND IS HYDROLYZED AND MEDIATES THE
 CC COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE.
 CC -1- SUBUNIT: MONOMER; DISULFIDE-LINKED.
 CC -1- SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,
 CC INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
 CC PIR: S23971; S23971.
 DR InterPro: IPR001599; Macroglobulin2.
 DR Pfam: PF00207; A2M; 1.
 DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
 KW Serine protease inhibitor; Glycoprotein; Plasma; Bait region.
 FT NON_TER 1
 FT THIOLEST 1
 FT NON_TER 5
 FT THIOLEST 8
 SQ SEQUENCE 18 AA; 2011 MW; D8D61C473D901C9D CRC64;

Query Match 29.7%; Score 19; DB 1; Length 18;
 Best Local Similarity 36.4%; Pred. No. 1.7e+03;

Matches 4; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 OY 2 PQGIACORNFN 12
 Db 2 PSCGEGQNMNIN 12

RESULT 14
 OXYT_RAJCL STANDARD; PRT; 9 AA.
 ID OXYT_RAJCL
 AC P42994;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Glutitocin.
 OS Raja clavata (Thornback ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalea; Hypnosqualea; Pristiogaster; Batoidae;
 CC Rajiformes; Rajidae; Raja.
 OX NCBI_TaxID=7781;
 RN [1]
 RP SEQUENCE:
 RA MEDLINE-66123415; PubMed=5880565;
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
 RT "Phylogeny of neurohypophyseal peptides: Isolation of a new hormone,
 RT glutitocin (Ser 4-Gln 8-ocytocin) present in a cartilaginous fish,
 RT the ray (*Raja clavata*)."
 RL Biochim. Biophys. Acta 107:393-396(1965).
 CC -1- FUNCTION: ANTIDIURETIC HORMONE.
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR InterPro: IPR000981; Neurohyp-horm.
 DR Pfam: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DSUFLEID 1
 FT MOD_RES 9
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 984 MW; 17E9C76B455B04B CRC64;

Query Match 28.1%; Score 18; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PQG 4
 Db 7 PQG 9

RESULT 15
 CEPL_ACHFU STANDARD; PRT; 11 AA.
 ID CEPL_ACHFU
 AC P22790;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Cardio-excitatory peptide-1 (ACEP-1).
 OS Achatina fulica (Giant African snail).
 OC Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Achatinacea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE:
 RC STRAIN-Ferussac; Tissue=Heart atrium;
 RX MEDLINE-90211261; PubMed=2322251;
 RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
 RT "A novel cardio-excitatory peptide isolated from the atria of the
 RT African giant snail, *Achatina fulica*.";
 RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
 CC -1- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO
 CC EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL
 CC MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE
 CC MOVEMENT OF ACHATINA.
 CC -1- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
 CC PIR: A34662; A34662.

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KW Hormone: Amidation. 11 AMIDATION.
FT MOD RES 11
SO SEQUENCE 11 AA; 1305 MW; 82D6D5B9C741365 CRC64;

Query Match 28.18; Score 18; DB 1; Length 11;
Best local similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 POG 4
111
Db 7 POG 9

Search completed: May 16, 2003, 10:37:29
Job time : 12 secs